

BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23

Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)  
 Subject: gi|4557225 ref|NP\_00005.1| alpha-2-macroglobulin precursor sp|P01023|A2MG\_HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M) pir|MAHU alpha-2-macroglobulin precursor - human >gb|AAA51551.1| (M11313) alpha-2-macroglobulin precursor [Homo sapiens] (SEQ ID NO: 23)  
 Length = 1474

Score = 2714 (960.4 bits), Expect = 1.7e-281, P = 1.7e-281  
 Identities = 596/1494 (39%), Positives = 874/1494 (58%)

Query: 13 LLLGMALSPAAELPNLYLVTLPARLNPFPSVQVKCLLSPGYSDVKFTVILETKDKTQK 192  
 Sbjct: LLL +L ++ + P Y+V +P+ L+ + +K C+ LS V + +LE+ +  
 Sbjct: 14 LLLLVLPTDASVSGK-PQYMLVPLPSLILHETTEKGCVLLSYLNFTVTVSASLESVRGNRS 72 ,

Query: 193 LLEYSGLKKRHLHCISFLVPPAGGTEEFAYATIRVSGVGNNISSFEKKVLIIQRQNGTFV 372  
 Sbjct: L + LHC+F VP + EEV + V G F+++ V+++ + + FV  
 Sbjct: 73 LFTDLEAENDVLHCVAFAVEK-SSSNEEVMFLTVQ/KGPTQEFFFKRRTVMVKNEDSLVFV 131

Query: 373 QTDKPLYTPGQQVYFRIVTMDSNFVPYNDKYSNVELQDPNSNRIAQWLEVVPEQGIVDLS 552  
 Sbjct: QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NR IAQW E G+ S  
 Sbjct: 132 QTDKSIYKPGQTVKFRVVSMDENPHPLNELIPLVYIQDPKGNRIAQWQSFSQLEGGLKQFS 191

Query: 553 FQLAPEAMLGTYTVAE--GKTFGTTSVEEYVLPKFKVVEVVPKELSTVQESFLVKIC 723  
 Sbjct: F P L+ E G+ Y V V + C+T F+V/E+VLPKF+V+V PK ++ +E V +C  
 Sbjct: 192 FPLISSEPFQGSYKVVVQKKSGGRTEHPFTTVEFLPKFEVQTVTPKLIITILEEMNVSVC 251

Query: 724 CRYTGKPMGLAVQVSVQCOKANTYWREREQLPDKCRNLSGQTDKTGCFSAPVDMATE 903  
 Sbjct: YYTGKP+ G V VS+C+K + E C SGQ + GCF V F  
 Sbjct: 252 GLYTGKPVPGHVTVSICRKYSDA--SIDCHGEDSQAFCEKFGQLNSHGCFYQQVKTKVF 309

Query: 904 DLIGAYASHQINITAVVVEEGTGYEANATONIYIISPQMGSMTFEDTSNFYHNPFPFSGKI 1.083  
 Sbjct: L Y +++ A + EEGT VE Q+ I+ + +F + + PF G++  
 Sbjct: 310 QLKKEYEMKLHTEAQIQQEGTVVUELIGRSSEITRTITKLSVKVDSHFRQGIPFFGQV 369

Query: 1084 RVRGGHDSFLKNHVLVFLVYGTNGTFNQTLVTDNNGLAPFTLETSGWMNGTDSLEGKFQM 1.263  
 Sbjct: R+ + N ++F I G + TD +GL F++ T+ GT +++ +  
 Sbjct: 370 RLVDGKGVPIPNKVIF--IRGENEANYSSNATTDEHGLVQFSINTTNVMGTSLSLTVRVNYYKD 427

Query: 1264 EDLVYNPEQVPPFYYQNAYLHLRPFYSTRSFLGLTHRLNGLPKCQGPQEVLVDYYIDPADA 1443  
 Sbjct: Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++  
 Sbjct: 428 RSPCYGYQWVSEEEETEAHHHTAYLVFSPKSKSFVHLEPMSHELPGHTQTQVQAHYILNGGTL 487

Fig 1A

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

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Query:	1444	SPDQEISFSYYLIGKGSLYMEQKHNLSKKGLKASFSLSLTFTSRЛАPDP SLVIAIFP +++SF Y ++ KG +V G L K++ 'K FS+S+ S +AP L+IY+A+ P	1623
Sbjct:	488	IGLRKLSFYYLIMAKGGIVRTGTHGLLVQEDMKGHFSISIPVKSDIAPVARLLIYAVLP	547
Query:	1624	SGGVVADKLQFSGVNCEDNQYSLGFSPSQQLPGAEEVLOQAAPGSLCALRAVDESVLL +G V+ D ++ V C N+V L FSPSQ LP + L++ AAP S+CALRAVD+SVLL+	1803
Sbjct:	548	TGDVIGDSAKYDVENCILANKVDSLSSPSQSLPASHAHLRVTAAPSVCALRAVDQSVLIM	607
Query:	1804	RDPRELSNRSYVYGMFPEWYGHYPYQVAEYDQCPCVSGPMDPQLIDPMPOGHSSQRSITW +ED ELS SVY + E D GP + Q D + + I +	1983
Sbjct:	608	KPDAELSSASSYNNLLP-----EKDLTGFPGPLN-DQDDDECDCINRHNVYINGITY	655
Query:	1984	RP-SFSEGTIDLFSFFRDVGLKILSNAKIKKPVDCSH-----RSPE-----YSTAMGGG P S + D+SF D+GLK +N+KI+KP C PE Y + + G	2124
Sbjct:	656	TPVSSNTNEKDVKYSSFLEDMGLKAFNTNSKIRPKPMCPQLQQYEMHGPPEGLRVGFYESDVMGR	715
Query:	2125	GHPEAFESSPLHQAEQDSQVQYQFPETWLMDLFPIGNSGKEAVHVTVPDAITEWKAMSFC GH P H VR+YFPETW+WDL + +G V VTVPD ITEWKA +FC	2304
Sbjct:	716	GHARLYVHEEP-HT--ETVTKYKFPETWIDLVVVNSAGVAEVGVTVPDTITEWKGAFIC	771
Query:	2305	TSQ5TRGFGLSPTVGLTAKPFVFDLTLFYSVVRGESFRLTATIFNYLKDCIRVQTDLAKS S+ G G+S T L AF+PFFV+LT+PYSV+RGE+F L AT+ NYL CIRV L S	2484
Sbjct:	772	LSEDAGLGISSSTASLRAFQOPFFVELTMPYSVIRGEAFTLKATVNLNYLKCIRVSVQLEAS	831
Query:	2485	HEYQLESMADSQTSSCLCADDAKTHHWNTTAVKLGHINFHTISTKILDNSEPCCGGQKGFPV + Q C+CA+ +T W +T LG+ +NFT+S + L+S E CG + VP	2664
Sbjct:	832	PAFLAVPVEKEQAPHCICANGRQTVSWAVTPKSLGNVNFTVSAEALESQELCGTEVPSVP	891
Query:	2665	QKGRSDTILIKPVLUVKPECVLVEKTHSSLLCPKGKVASESVSLELPVDIVPDSKAYTVL + GR DT+IKP+LV+PEG+ E T +SLLCP G SE +SL+LP + +V +S +A V+VL	2844
Sbjct:	892	EHGRKDTVVIKPLLVEPEGLEKETTFNSLLCPGGEVSEELSLLKLPVNVEESARASVSVL	951
Query:	2845	GKOLEILDSERKRMRMEEAKVWRDIMGTAQNLDGLVQMPGCGEOQMVLFAPIIYTQYL G DI+G+A+ON L+QMP GCGEQNMVLFAPIIYTQYL	3024
Sbjct:	952	G-----DILGSAMQNTQNLQMPYGCGEQNMVLFAPIIYTQYL	990
Query:	3025	EKAGLLTEIRSRAYGFLIEGYQKELMYKHSNGSYSAFGERDGН--GNTWLTATVTKCFG + LT E++S+A+G+L GYQ+L YKH +GSYS FGER G GNTWLTAFV K F	3198
Sbjct:	991	NETQQLTPPEVKSKAIGYLNTGYQRQLNQYHYDGSYSTFGERYGRNQGNTWLTAFVLTAFVA	1050

**Fig. 1B**

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR SEQ ID NO: 23**

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Query:	3199	QAQKFIIDPKNIQDAALKWMAGNOQLPSCGYANVGNILLHTAMKGVDDEVSLTAYVTAALL	3378
Sbjct:	1051	QA+ +I AL W++ Q +GC+ + G+L+ A+KGGV+DEV+L+AY+T ALL	1110
Query:	3379	EMGKDVIDDPMSQGLRCKNSATST-----ITNL-YTOAIIAYIFSLAGEMDIRNLLKQ	3537
Sbjct:	1111	E+ V P++ L CL+ SA T +++YT+ALLY F+LAG D R +LK	1169
Query:	3538	LDQQQATLGSSEIYWSQKPTPSNAPWSEPA--V-DVELTAYALLAQLT-KPSLTQKEIA	3708
Sbjct:	1170	L+++A+ S++W + P + EP A +VE+T+Y LLA LT +P+ T +++	1229
Query:	3709	KATSIVAWLAKOHNAYGFSSTQDTTVVALQALAKY-ATTAYMPSEEINLVVKSTENFORT	3885
Sbjct:	1230	AT+IV W+ KQ NA GGFSSSTQDTTVVAL AL+KY A T + + ++S+ F	
Query:	3886	FNIQSVAIRLVQQDTLPNVPGMYTLEASGGCVYVQTVLRYNILPPTNMKTFSLSVELRK	4065
Sbjct:	1290	F+ + NRL+ QQ +LP +PG Y++ +G+GCYX+OT L+YNILP F+L V+ FQVDNNNRLLLQQVSILPELPEGEYSMKVITGEGVYLQTSLKYNILPEKEEFPFALGVQTLIP	1349
Query:	4066	ARCEQPTSPRSLTLTHTSYVGSRSSNNMAIVEVKMLSGFSPMEGTNQLLQQPLVVKVE	4245
Sbjct:	1350	C++P + S +++ SY GSRS+SNMATE+VRM+SGF P++ T +L + V + E QTCDEPKAHTSFQISLSVSYTGSRASNSMAIVDVKMVSQFIPLKPTVKMLERSNHVSRTE	1409
Query:	4246	FGTDITLNTYLDDELTKNTQTYTFTISQSVLVTNLKPATIKVYDYLPGSFKLSQLY	4407
Sbjct:	1410	++ + IYLD++ T + FT+ Q V V +LKPA +KVYDYY F ++Y VSSNHVLIYLDKVSNQTLSSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFAIAEY	1463

**FIG. 1C**

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 4)  
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. (SEQ ID NO 24)  
 Length = 1474

Score = 2699 (955.2 bits), Expect = 3.2e-280, P = 3.2e-280  
 Identities = 596/1494 (39%), Positives = 870/1494 (58%)

Query:	13	ILLGMIALSPATAEELPVNLVTPARLNFPSSVQKVCLDLSPGYSDVKFTVTLETDKKTQK	1.92
Subject:	13	LLL +L + A P Y+V +P L+ + +K C+ LS V + +LE+ +	
Query:	193	I LEYSGLKKRHLHCISFLVPPPAGGTEEVATIRVSGVGNNTISFEKKKKVLIQRGNGTTFV	3.72
Subject:	73	L + LHC++F VP + EEV + V G F+++ V+++ + + FV	
Query:	373	QTDKPLYTPQQYVTRIYTMDSNFVYNDKYSMVELQDPNSNRIAQWLEVPEQGVVDLS	5.52
Subject:	132	QTDK +Y PGQ V FR+A+MD NF P+N+ +V +ODP NRIAOW E G+ S	
Query:	553	FOLAPEAMLGTYTVAE -- -GKTFGTFSVEEYVLPKFKVVVEPKELSTVQESFLVKIC	7.23
Subject:	192	F PLSSSEPQGSYKVVVQKSSGGRTHEPFTVFEFLPKFEVQVTVPKITITLEEMMVSYC	2.51
Query:	724	CRYTYGKPMGLGAVQSTVQCKANTYYREVEREQLPDKCRNLSGQZDKTKGCSAPVDMATF	9.03
Subject:		YTYGKp+ G V VS+C+K + + E C SGQ + GCF V F	
Query:	252	GLYTGKPKPGHVTVSICKYSDA -- SDCHGEDSQAFCEKFSGQNLNSHGCFYQQVKTVF	3.09
Subject:		3 L Y +++ A + EEGT VE Q+ I+ + ++F + + PF G++	
Query:	904	DLIGYAYSHQINIVATVVEGTGEANATQNIYISPOQMSMTFEDTSNMFYHPNFPFGSKI	10.83
Subject:		252 GLYTGKPKPGHVTVSICKYSDA -- SDCHGEDSQAFCEKFSGQNLNSHGCFYQQVKTVF	
Query:	310	QIKRKEYEMLHTEAQIQEETVVELTGRQSSETTRITKLTSFVVKDHSFRQGIPFTFGQV	3.69
Subject:		310 QIKRKEYEMLHTEAQIQEETVVELTGRQSSETTRITKLTSFVVKDHSFRQGIPFTFGQV	
Query:	1084	RYRGHDSSFLKMHLVFLVIYGTNGTFNQTLVTDNNGLAPFTLETSGWNGBTDSLECFXFM	12.63
Subject:		R+ + N ++F I G + TD +GL F++ T+ GT +++ ++	
Query:	370	RLVDGKGKGPPIPKNVIF -- IRGNEANYYNSNATTDEHGLVQFSINTNNMGTSLTVNYKD	4.27
Subject:		370 RLVDGKGKGPPIPKNVIF -- IRGNEANYYNSNATTDEHGLVQFSINTNNMGTSLTVNYKD	
Query:	1264	EDLYVNPEQVPRYYQAYYLHLPFYSTTRSFLGIHRLNGPLKCGQPOQEBYLVDYYIDPADA	14.43
Subject:		Y + V ++ A+ +S ++SF+ + ++ L CG Q V Y ++	
Query:	428	RSPCYGYQWVSEEEAHHTAYLFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTL	4.87
Subject:		428 RSPCYGYQWVSEEEAHHTAYLFSPSKSFVHLEPMSHELPCGHTQTVQAHYILNGGTL	
Query:	1444	SPDQEISFSYYLIGKGSILVMEGQKHLNSKKGLKASFSLTLFTSRLAPDPSLVIYAIIFP	16.23
Subject:		++SF Y ++ KG +V G L K++ +K FS+S + ++ L +IYA+ P	
Query:	488	LGLKKLSSLFYYLIMAKGGIVRTGTHGLLVQEDMKGHFSTISIPVRSIDLAPVRLIYAVLP	5.47
Subject:		488 LGLKKLSSLFYYLIMAKGGIVRTGTHGLLVQEDMKGHFSTISIPVRSIDLAPVRLIYAVLP	

**Fig. 2A**

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query:	1624	SGGVVADKIQFSVGMCFDNQVSLGHSPSQLPGAEVELQLQAAPGSLCALRAVDESSVLL	1803
Sbjct:	548	+G V+ D ++ V C N+v L ESPSQ LP + L++ AAP S+CALRAVD+SVLL+	607
Query:	1804	RDPRELNSNRSVYGMFPFWYGHYPYQYAEDQCPVSGPWFDFPQPLIDPMQGHSSQRSSIW	1983
Sbjct:	608	+PD ELS SVY + P E D GP + Q D + + + I +	655
Query:	1984	RP-SFSEGTDLFLSFRRDGLKILSNAKRKPKVDCSH-----RSPE-----YSTAMGGG	2124
Sbjct:	656	P S + D+SF D+GLK +N+K+I+K P C PE Y + + G	715
Query:	2125	GHPFAFESSTPLHQAEQDSQVRYQFPETLWDLFPIGNSGKEAVHVTVPDAITEMKAMSFC	2304
Sbjct:	716	GH P H VR+YF ETW+MDL + ++G V VTVPD ITEWKA +FC	771
Query:	2305	TQSRSRGFGLSPSTVGLTAAFKPFVFVDTLPLYSVVRGESFRLTATIFNYLKDCIRVQTDLAKS	2484
Sbjct:	772	S+ G G+S T L AF +PFFV+LT+PSV+RGE+F L AT+ NYL CIRV L S	831
Query:	2485	HEYQLESWADSQTSSCLCADDAKTHWNNTAVKLGHINFTISTKILDNEPCGGQKGFVP	2664
Sbjct:	832	+ Q C+CA+ +T W +T LG++NFT+S + L+S E CG + VP	891
Query:	2665	QKGRSDTTLIKPVLYKPEGVLVEKTHSSLLCPKGKVASESVSLELPVDIVPDSKAYVTVL	2844
Sbjct:	892	+ GR DT+IKP+LV+PEG+ E T +SLCP G SE +SL+LP ++V +S +A V+VL	951
Query:	2845	GKQLEILDSEKRMRMEEAKVWRDIMGTAQNLDGLVQMPGCGEQNMLFAPLIYVLOYL	3024
Sbjct:	952	G DI+G+A+ON L+OMP GCGEQNMLFAP TYVL YL	990
Query:	3025	EKAGHLTEEIRSRAVGFLEIGYOKELMYKHSNGSYSAFGERDGNN-GNTWLTAFVTKCFG	3198
Sbjct:	991	+ LT ET+S+A+G+L GYQ+L YKH +GSYS FGER G GNTWLTAFV K F	1050
Query:	3199	QAQKFIFIDPKNIQDALKMAGNQLPSGCYANVGNNLHTAMKGGVDEVSILTAYVTAALL	3378
Sbjct:	1051	QA+ +IFID +I AL W++ Q +GC+ + G+LL+ A+KGGV+DEV+L+AY+T ALL	1110

**Fig. 2B**

**BLASTX ALIGNMENT OF SEQ ID NO: 4 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query:	3379	EMGKDVEDDEPMVSQGLRCLKNSATST-----TNYTQALLAYIFSLAGEMDIRNILLKQ	3537					
E+	V	F+V	L CL+	SA	T	+++YT+ALLY F+LAG	D R +LK	
subjct:	1111	EILLTVTHEVVRNALFCLE-SAWKTTAQUEGDHGSHVYTKALLAYAFALAGNQDKRKVELKS	1169					
Query:	3538	LDQQAILISGESETYWSQRKPTPSSNAPWSEPA--V-DVELTAYALLAQLT-KPSLTQEKEIA	3708					
I+++A+	S++W	P	+ EP A	+VE+T+Y	LLA LT +P+ T	+++		
subjct:	1170	INEEAVKKDNDSVHMERQKPKAPVGHFYEPOAPSAAEVEMTSYVLLAYLAQPASTDLT	1229					
Query:	3709	RATSIWAMIAKQHNAYGGSSSTQDTIVVALQALAKY-ATTAYMPSEEINUVKSTENFQT	3885					
AT+IV	W+	KQ NA GGPSSSTQ	TIVVAL AL+KY	A T	+	++S+	F	
subjct:	1230	SATNIVVKWITKQONAQQGFSSTQHTIVVALHALSKYGAATFRTGKAQVTIQSSTGFSSK	1289					
Query:	3886	ENIQSVANRLVFQQDTLIPNVPGMITYLEASGOGCVVYVQTVLRYNILPPTNMKTFSLSVIEIGK	4065					
F	+	NRI+	QQ	+LP	+PG Y++	+G+GCYY+OT	L+YNILP	F+L V+
subjct:	1290	FQVDNNNNRLLQQVSLPELPGEYSMKVTGCVYLQTSILKYNILPEKEEFFPALGVQTLP	1349					
Query:	4066	ARCEQPTSPRSILTITHTSYVGSRSSSNMAIVEVKMLSGFSPMEGTNQQLLQQPLVVKVE	4245					
C++P	S	+++	SY	GSRs+SNMAIV+VCRM+SGF	P++ T	++L	+ V	+ E
subjct:	1350	QTCDEPKAHTISFQIISLSVSYTGSRSASNMAIVDVKMVSGFIPLKPTVKMLERSNHVSRTE	1409					
Query:	4246	FGTDLNLINYLDLTIKNTQTYTFTTISQSVLVTNLKPATIKVYDYYLPGSFKLSQLY	4407					
++	+ TYLD++	T	+ FT+	Q V	V +LK PA	+KVYDYY	F	+++Y
subjct:	1410	VSSNHAVLIVLDKVSNCUSSLFFTVLQDVPVRDLKPAIVKVYDYYETDEFATAEY	1463					

**FIG. 2C**

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH OVOS\_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

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Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)  
Subject: >sp|P20740|OVOS\_CHICK OVOSTATIN PRECURSOR (OVOMACROGLOBULIN) >pir|IA20872 ovostatin precursor - chicken  
>emb|CAA55384.1| (X78801) ovomacroglobulin, ovostatin [Gallus gallus] (SEQ ID NO: 41)  
Length = 1473

Score = 1300 (462.7 bits), Expect = 6.1e-135, Sum P(2) = 6.1e-135  
Identities = 297/849 (34%), Positives = 457/849 (53%), Frame = +3

Query: 96 VYKFPVSPDKMWAQLLGMIALSPAIAEEL-PNVLVTLPARLNFPSVQKVCLDLSPGYS 272  
+ F ++ KMW + +L L A +E P Y++ +PA L S +VCL  
Sbjct: 9 ILSFFCLTVRKMLKFLAILLHAAGKEPEPQYVLMMPAVLQSDSPSQVCLQFFNLNQ 68

Query: 273 DVKFTVTLTLETKDTQKLLYESGLKRRHLHC1SFVLPVPPAGTEEVATIRVSGVGNNISFE 452  
+ V LE + E + L C+F++PP + +A I + G +  
Sbjct: 69 TISRVVILEYDTINTTIEFKNTTTSNGLQCLNFMIPIPVT-SVS LA FISFTAKGTTFDLK 126

Query: 453 EKKKVLIIQRQNGNTFVQTDKPLLYTPGQQVYFRIVTMDSNFPVNNDKYSMVELQDPNSR I 632  
E++ V+I + FVQTDKP+Y PGQ V FR+V +D NF PV + Y ++ +QDP +NR I  
Sbjct: 127 ERRSYMTWNAMESFVYQTDKPIYKPGQSYMFRRVALDFNFKPVQEMYPLIAVQDFQNRI 186

Query: 633 AQMLEVVPEQGVIDLSQLAPEAMLGTYTVAAE--G-KTFGTFSVEEYVL.PKEFKEVVE 803  
QW V E IV + F L E +LG Y + V + G +T +F VEYYVL.PKF V V  
Sbjct: 187 FQWQNYTSEINIVQLEIFPLTEEPILGNYKIIIVKKSGERTSHSFLVEYYVL.PKFDTVTA 246

Query: 804 PKELSVYQESFLVKICCCRITYGKPMGLAVQVSVCQKANTYWWREVEREQLPDKCRNLSGQ 983  
P L+ + VKIC YYG+P+ G VQ+SVC+ +Y R + C++ +  
Sbjct: 247 PGSLTVMDSELTVKICAVVYTGQPEGKVQLSVCRDFDSYG----RCKKSPVCQSFRKD 301

Query: 984 TDKTGCFSAVPDMATFDLIGYAYASHQINITAVVEEGTGVANATQNIYISPMQGMFIE 1163  
D GC S + F+L Y +++ A V E+ ATQ+I I+ M S+ FE  
Sbjct: 302 LDTDGCLSHILSSKVFEILNRIGYKRNLDVKAIVTEKEQVCNLTATOSISITQYMSLQFE 361

Query: 1164 DTSNFYHPNFPFSGKIRVRGHDDSFLLKNHLVFLVIYGTNGTFNOTLVTDINGLAFILET 1343  
+ + Y P+ G+I++ D+S + N ++ L + N T N T TD NG+APF++T  
Sbjct: 362 NVDDHHYRG1PYFGQ1KLVDKDNSPISNKKV1QLFVNKKN-THNFT-TDINGIAPPSTDT 418

**Fig 3A**

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH  
OVOS\_CHICK OVOSTATIN PRECURSOR SEQ ID NO: 41**

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Query:	1344 SGWNGTDSLEGKFQMFEDLVYNPEQVPRYYQAYLHLRPFYSTTRSFGLGIHRLNGLPKCG	1523
Sbjct:	419 SKIFDPELSKALYKTSDOCHSEGWIPEPSYDASLSVQRLLYSWTSSFVRIEPLWKDMSCG	478
Query:	1524 QPQEVLVDYYIDFADASPDQEITFSYYLIGKGSIVMEGQKLNSKKGLKASESLSLTFT	1703
Sbjct:	479 QRKRMITVYYTINTDEGYEHINTVNFYYYGMAKGKIVLTGEIKVNIQADQ-NGTFEMIPLVVN	537
Query:	1704 SRLAEPDSLVIYIAFPSSGGVIADKIQFSVEMCFDNQVSIGFSPSQLPQAEVELQLQAAP	1883
Sbjct:	538 EKMAPALRILVYMLHPAKELVADSVRFSLIEKCFKNKVQLQFSEKQMLTSNVSIVAAA	597
Query:	1884 GSICALRAVDDESVLLLRPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPWDFPQFL	2063
Sbjct:	598 NSFCAVRAVDKSMLLIKSETELSAETIYNLHPI----QDLQGYIFNLNLE---DDPQ--	648
Query:	2064 IDPMPQGHSS-QRSIWIWRPSFSE-GTDLFSFFRDVGGLKILSNAKIKKPVDCCSH---RSPE	2228
Sbjct:	DP + + + +RP S G D++ F RD+G+K +N+KI+P C+ R P	
Query:	649 -DPCVSSDDIFHKGLYTYRPLTSGLGPDVYQFLRDMGMKFFTNSKIRQPTVCTRETRVPPS	707
Sbjct:		
Query:	22229 YSTAMG--AGGGHPE----AFESTTPLHQAEQDSQVRYFPETWLWDLFPIGNSGKEAVH	2387
Sbjct:	Y G A H + A E H E +R+FPETW+WD+ I ++GR +V	
Query:	708 YTLNAGRTASTHVKLSAEVAREERGKRHILET--IREFFPETWIWDLILINSTGASVS	765
Sbjct:		
Query:	2388 VTVPEDAITTEWKAMSFCTSQSRGFGLSPTVGLTAFKPFFVVDLTLPSVWGESFRLTATIF	2567
Sbjct:	T+PD ITENKA +FC + GFGe+S LTAF+PFFVVDLTLPS+ GE F + A +F	
Query:	766 YTIPDTITTEWKASAFCVEELAGFGMSVPATLTAQPFVVDLTLPSITHGEDFLVRANVF	825
Sbjct:		
Query:	2568 NYLKDCIRV 2594	
Sbjct:	NYL C+ +	
Query:	826 NYLNHCII 834	

**Fig 3B**

**BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24**

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Query: Alpha-2-macroglobulin polypeptide (SEQ ID NO: 29)  
 Subject: sp|R11334|R11334 Recombinant human alpha-2 macroglobulin. SEQ ID NO: 24  
 Length = 1474

Score = 1289 (458.8 bits), Expect = 5.6e-134, Sum P(2) = 5.6e-134  
 Identities = 300/834 (35%), Positives = 448/834 (53%), Frame = +3

Query: 141 ILLGMIALSPAELPNVYLTLPARLNFPSSQKVCLDLSPGYSVDKFTVTLETDKTQK 320  
 ILL +L + A P Y+V +P+ L+ + +K C+ LS V + +LE+ +  
 Sbjct: 13 ILLVLVPTDASVGKPKQYMLVPSLHETTERGCVLLSYLNETVTVSASLESVRGNRS 72

Query: 321 ILEYSGLKKRHLHCISFLVPPAGGTTEAVATIRVSGVGNNIISFEKKKKVLIQRQGNGTGV 500  
 L + LHC++F VP + EEV + V G F+++ V+++ + + FV  
 Sbjct: 73 IFTDLEAENDVLHCVAFAPK-SSSNEEVMFILTVQVKGPTQEFKKRRTVMVNEDSLVFV 131

Query: 501 QTDKPLIYTRPGQQYYFRYVYTMDSNFVYNDKYSMVELQDPNSNRIAOWLEVPEQGIVLDS 680  
 QTDK +Y PGQ V FR+V+MD NF P+N+ +V +QDP NRIAOW E G+ S  
 Sbjct: 132 QIDKSIVYKPGQTVKFRVVSMDENFHPLNELIPLVYIQDPKGNRIAQWQSFLQEGGLKQFS 191

Query: 681 FOIAPEAMLGTYTVAEE--GKTFGTFSVEEYVLPKFKVVEVVPKELLSVQESFLVKIC 851  
 F L+ E G+Y V V + G+T F+VEE+VLPKF+V+V PK ++ ++E V +C  
 Sbjct: 192 FPLSSEPFQGSYKVQKSGGRTEHPFTVEFVLPKFEEVQTVPKIITLLEEMNVSVC 251

Query: 852 CRYTYGKPEMLGAVQVSVCQKANTWYREVEREQLPDKCRNLSGQTDDKGCSAPVDMATE 1031  
 YTYGKP+ G V VS+C+K + E C SGQ + GCF V F  
 Sbjct: 252 GLYTGYGKPVPGHVTVICRKYSDA--SDCHGEDSQAFCEKFSQQLNSHGCFYQQVKTKVF 309

Query: 1032 DLIGAYASHQINIVATVVEEGTGVANATONLYISPQMGSTMFEEDTSNIFYHBNFPESGKI 1211  
 Sbjct: 310 QLKKEYEMKLHTEAQIQQEETVVELTGROSSEITRTITKLSFVKVDSHERQGIPFFGQV 369

Query: 1212 RYRGHDDSFILKNHLVFLVIYGTNGTIFNQTLVTDNNGLAPFTLETSGWNGTDXLEGKFQM 1391  
 R+ + N ++F I G + TD +GL F++ T+ GT +++ ++  
 Sbjct: 370 RLVDGKGKVPIPINKVIF-IRGNEANYYSNATTDEHGLVQFSINTNTVNGTSLTVRNLYKD 427

Query: 1392 EDLVNPEQVPRYYQAYLHLRPFYSTTRSFLGIHRINGLKCQGQEQFLVDYYIDPADA 1571  
 Sbjct: 428 RSPCYGYQMVSEEHEEAHTAYLFSPSKSFVHLEPMSHELLPCGHTQAHYILLNGGTL 487

**Fig. 4A**

BLASTX ALIGNMENT OF SEQ ID NO: 29 ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDE WITH RECOMBINANT HUMAN ALPHA-2-MACROGLOBULIN SEQ ID NO: 24

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Query: 1572 SPDQEISFSYYLIGKGSIVMEGQKHILNSKKKGUKASFSLSLTFTSRALAPDPSLVIYALIFP 1751  
Sbjct: 488 LGLKKLFSFYLIIMAKGGIVRTGTHGLLVQEDMKGHFSISIPVKSDIAFPVARLLIYAVLP 547

Query: 1752 SGGVVAADKIQFSVEMCNDNQVSIGRSPSSQLPGAEVELQIQAAPGSLCALRAVDESVILL 1931  
Sbjct: 548 TGDVIGDSAKYDVENCCLANKVDSLSPSQSLPASHAHLRVTTAAPQSVCALRAVDQSVLIM 607

Query: 1932 RPDRELSNRSVYGMFPFWYGHYPYQVAEYDQCPVSGPMPQHSSQRSIIW 2111  
Sbjct: 608 KPDAAELSSASSVNLIP-----EKDLTGFPGPIN-DQDDDECINRNHNVYINGITY 655

Query: 2112 RP-SFSEGIDLFLSFPRDYGLKLTSNAKIKKPVDCSH-----RSPE-----YSTAMGAG 2252  
Sbjct: 656 P S + D+SF D+GLK +N+KI+KP C PE Y + + G  
TPVSSTNEKDMDMYSFLEDMGKKAFTNSKIRKPKMCPOLQQYEMHGPEGLRVGFYESDV-MG 714

Query: 2253 GHGHPEAFESSSTPLHQAEQEDSQVRQYFPETWLMDFPIGNSSKEAVHVTVPDAITEWKAMSF 2432  
Sbjct: 715 FGHARLHVHEEP-HT---ETVRKYFAETWIWDLVVVNSAGVAEVGVTPDTITEMKAGAF 770

Query: 2433 CTSQSRGFGELSPPTVGLTAKPFFVVLTLPSYSVVRGESFRRLTATIFNYLKCIRV 2594  
Sbjct: 771 CLSEDAGLGISSSTASLRAFQOPFFVVELTMPYSVIRGEAFTLKVTLNYLPKCIRV 824

**Fig. 4B**